

Result No.	Score	Query Match Length	DB ID	Description
1	21.4	82.3	431	BB032631
2	21.4	82.3	616	A_453025
3	3.0	86.6	673	A_471605
C	4	20.6	79.2	NS0104
C	5	20.4	78.5	CNS0104
C	6	20.2	79.0	17
		77.7	80.4	A771348C
SUMMARIES				
8				
<p>ON nucleic - nucleic search using SW model</p> <p>Run on: Jacaru 14 2003 11:42:22 - Search type 11:17 seconds (without alignments) 11136.303 Million cell updates/sec</p> <p>Title: US-19-910-428-2</p> <p>Perfect score: 26</p> <p>Sequence: 1 ccccccacatcaatatttttc 26</p> <p>Scoring table: IDENTITY_NUC</p> <p>Gapop 10.0 , Gapext 1.0</p> <p>Searched: 16154066 seqs, 8097743376 residues</p> <p>Total number of hits satisfying chosen parameters: 32308132</p> <p>Minimum DB seq length: 0</p> <p>Maximum DB seq length: 2100000000</p> <p>Post-processing: Minimum Match 0.8</p> <p>Maximum Match 100%</p> <p>listing first 45 summaries</p> <p>Database :</p> <p>EST: *</p> <ol style="list-style-type: none"> <li>1: em_estba: *</li> <li>2: em_esthum: *</li> <li>3: em_estin: *</li> <li>4: em_estmu: *</li> <li>5: em_estov: *</li> <li>6: em_estpl: *</li> <li>7: em_estro: *</li> <li>8: em_hic: *</li> <li>9: qb_est1: *</li> <li>10: qb_est2: *</li> <li>11: qb_htc: *</li> <li>12: qb_est3: *</li> <li>13: qb_est4: *</li> <li>14: qb_est5: *</li> <li>15: em_estfun: *</li> <li>16: em_estom: *</li> <li>17: qb_gss: *</li> <li>18: em_gss_hum: *</li> <li>19: em_gss_inv: *</li> <li>20: em_gss_pln: *</li> <li>21: em_gss_vrt: *</li> <li>22: em_gss_fun: *</li> <li>23: em_gss_mam: *</li> <li>24: em_gss_mus: *</li> <li>25: em_gss_mur: *</li> <li>26: em_gss_pro: *</li> <li>27: em_gss_rod: *</li> </ol> <p>pred. No. is the number of results predicted by chain, to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.</p> <p>ALIGNMENTS</p> <p>RESULT 1</p> <p>LOCUS RH032631 DEFINITION RP1-24-239N18.TV RP1-24 Mus musculus genomic clone RP1-24-239N18</p> <p>ACCESSION BH032631</p> <p>VERSION BH032631.1 GI:14803637</p> <p>KEYWORDS GSS</p> <p>ORGANISM Mus musculus</p> <p>REFERENCE 1 (basses 1 to 431)</p> <p>AUTHORS Zhao,S., Nieman,W., Malek,J.J., Shatsman,S., Akintoye,B., Levins,M., Tsehai,S., Juett,K., Kiel,M., Shavit-Shayev,A., Schlegelofis,E., Russell,D., de Jong,P. and Fraser,C.M.</p> <p>TITLE Mouse BAC End Sequences from Library RP1-24</p> <p>COMMENT Unpublished (1999)</p> <p>Contact: Shaving Zhao</p> <p>Department of Eukaryotic Genomics</p> <p>The Institute for Genomic Research</p> <p>9712 Medical Center Dr., Rockville, MD 20850, USA</p> <p>Tel: 301 838 0200</p> <p>Fax: 301 838 5408</p> <p>Email: <a href="http://www.sra.wustl.edu">www.sra.wustl.edu</a></p> <p>Copies are derived from the mouse BAC library RP1-24. For BAC library availability, please contact Pieter de Jong (pijdejong@med.wustl.edu). Clones may be purchased from BACON.</p> <p>Copyright (c) 1993 - 2003 CompuGen Ltd.</p> <p>Genome version 5.1.3</p> <p>AW522881 UI-R-B00-AW523946 UI-R-B00-H1024260 UI-R-HSI-H20-BH03286 KIC1-24-2-AW73635913 KIC1-24-8-AW382229 IM0159415-AW331729 614056C01-A287765 2MC137G12-HQ198536 01-R-FHO-A2350728 1M0088H23-A0351507 RHC111-11-F323-7 RSE24973 H-F323-7 RSE24973 H-B0481609 PV_Gra005-AK012255 Mus muscu-AK011513 Tetradon-A15722 0d1192-r-A155053 1M040521-A025401 A0254604-AA200990 mu12910_r-A03211193 RHC111-11-A294632 2MC238P05-A2645945 mu12910_y-BQ57590 M1-P-A2-a-BH439410 BQXUW3TR-BH439410 BQXUW3TR-BH136123 60178573-H-130754 60178274-A054227 Drosophili-A054227 Drosophili-BE86944 601445395-BE86944 601445395-BU19296 RST18577-A2660399 1M053P23-BH418635 1M18635-A0209240 HS_3236_H-H4562940 HS_3236_H-BH417940 LINEST1H-A2350546 1M008B420-A1216914 Tetradon-BG246571 602360617</p>				









REFERENCE 1 (bases 1 to 587)  
AUTHORS zhang,S., Nierman,W., malek,I., shatsman,s., Almouz, R., levins,M.,

Tsatsas,G., Gru, K., Kral,M., Ghazalpour,A., deJong, E.,

Roussell,D., de Jong, P., and Fraser,G.M.,

TITLE Mouse BAC End Sequences from Library RPCI-24

COMMENT Unpublished (1999)  
Other\_GSS: RPCI-24-247H24.WJ

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The Institute for Genome Research

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Email: szhang@igr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mol.cho.oriq). Clones may be purchased from BACPAC Resources (<http://www.bacpac.org>). Order online from BACPAC Resources (<http://www.bacpac.org/order.html>) or by fax to 301-435-0741. Order online from BACPAC Resources (<http://www.bacpac.org/order.html>) or by fax to 301-435-0741. Seq primer: T7

Class: BAC ends.

FEATURES Location/Qualifiers  
Source

Organization="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_id="RPCI-24-B8K5"

/sex="Male"

/chromosome="X"

/contig="Vector\_PTBAC11"; Site\_1: Bam11; Site\_2: Bam11;

RPCI-24 Mouse BAC library produced by Pieter de Jong. The

library was cloned in the PTBAC11 cloning vector at the

Bam11 sites using MboI partially digested male C57BL/6J

DNA.

BASE COUNT 186 a 128 c 107 g 166 t

ORIGIN

Query Match 76.2%; Score 19,8; DB 17; Length: 587.

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 195 TCCGAACTTCAATTATTTCT 217

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

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Email: szhang@igr.org  
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FEATURES Location/Qualifiers

Source

1..635

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_id="RPCI-24-B8K5"

/sex="Male"

/chromosome="X"

/contig="Vector\_PTBAC11"; Site\_1: Bam11; Site\_2: Bam11;

RPCI-24 Mouse BAC library produced by Pieter de Jong. The

library was cloned in the PTBAC11 cloning vector at the

Bam11 sites using MboI partially digested male C57BL/6J

DNA.

BASE COUNT 153 a 125 c 133 g 224 t

ORIGIN

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

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Class: BAC ends.

FEATURES Location/Qualifiers

Source

1..635

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_id="RPCI-24-B8K5"

/sex="Male"

/chromosome="X"

/contig="Vector\_PTBAC11"; Site\_1: Bam11; Site\_2: Bam11;

RPCI-24 Mouse BAC library produced by Pieter de Jong. The

library was cloned in the PTBAC11 cloning vector at the

Bam11 sites using MboI partially digested male C57BL/6J

DNA.

BASE COUNT 153 a 125 c 133 g 224 t

ORIGIN

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

RESULT 12

AV382229

LOCUS

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0; Gaps: 0;

Version: 3

4 TCCGAACTTCAATTATTTCT 25

1b 36 TCCGAACTTCAATTATTTCT 14

Fax: 301 838 0208  
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Class: BAC ends.

FEATURES Location/Qualifiers

Source

1..635

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_id="RPCI-24-B8K5"

/sex="Male"

/chromosome="X"

/contig="Vector\_PTBAC11"; Site\_1: Bam11; Site\_2: Bam11;

RPCI-24 Mouse BAC library produced by Pieter de Jong. The

library was cloned in the PTBAC11 cloning vector at the

Bam11 sites using MboI partially digested male C57BL/6J

DNA.

BASE COUNT 153 a 125 c 133 g 224 t

ORIGIN

Query Match 76.2%; Score 19,8; DB 17; Length: 635;

Best Local Sim: 91.3%; Fred. No.: 4,1+0.2;

Matches: 21; Conservative: 0; MisMatches: 2; Indels: 0



base count and selected for ampicillin resistance. <sup>a</sup>

LARVUS  
 DEFINITION  
 BCI R EBO c1c-b-08 0 01 1 1 01 R EBO Rattus norvegicus DNA clone  
 ACCESSION  
 BCI99530  
 VERSION  
 BCI99530\_1  
 KEYWORDS  
 EST  
 SOURCE  
 ORGANISM  
 Rattus norvegicus

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 PAGENUMBER  
 COMMENT

Bonaldo, M. F., Leonor, G., and Soares, M. B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
*Genome Res.*, 6 (9), 791-806 (1996)  
 9704477

Contart, Soares, MB

/lab host-<sup>+</sup>OH10 (Life Technologies).  
 /note- Vector: pT7-5-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; HTP-EGO is a non-normalized Rat duodenum library (RBDL) constructed in pT7-19 vector according to the procedure described by Honjo, Lennon & Soares (Genome Research Genome 5: 791-808, 1996). The oligonucleotide used to prime first strand synthesis contained the sequence tag TGTGTTAT between the Not I cloning site and dT8 stretch. The Rat duodenum tissue was provided by Tom Freeman of the Sanger center.  
 TAG: 1,1,01 R EHO  
 TAT: TISSUE-duodenum  
 TAG: SEW-TGTGTTAT